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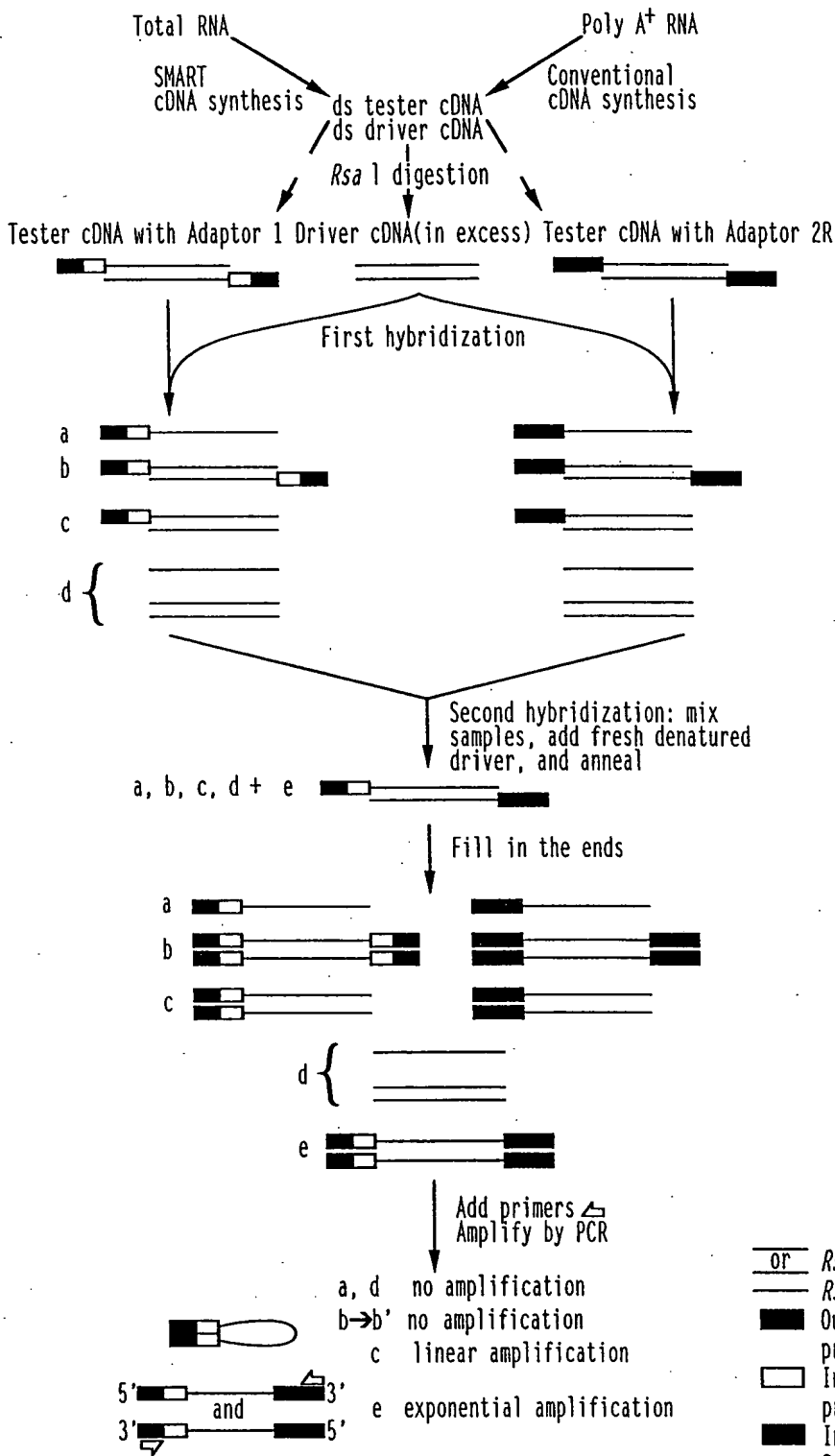
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FIG. 1



Prepare cDNA by either SMART or conventional synthesis.

Separately digest tester and driver ds cDNA to obtain shorter, blunt-ended fragments.

Divide tester cDNA into 2 portions and ligate each portion to a different adaptor. Driver cDNA has no adaptors.

Hybridization kinetics lead to equalization and enrichment of differentially expressed sequences among ss tester molecules.

Generate templates for PCR amplification from differentially expressed sequences.

Due to suppression PCR, only differentially expressed sequences are amplified exponentially.

- or Rsa I digested tester cDNA
- Rsa I digested driver cDNA
- Outer portion of adaptors/PCR primer sequence
- Inner portion of Adaptor 1/nested PCR primer 1
- Inner portion of Adaptor 2R/nested PCR primer 2R

mICACC-1 cDNA Translated Sequence
Sequence Range: 1 to 2931

FIG. 2A

```

1                                     ctgcagg

8  atggaatctttgaagagtcctgtcttcctcttgatcctccacctt
   M E S L K S P V F L L I L H L
53 ctggaaggagttctgagtgagtcctcatccaactgaacaacaac
   L E G V L S E S L I Q L N N N
98 ggctatgagggcatcgatcgccatagaccacgacgtgccggaa
   G Y E G I V I A I D H D V P E
143 gatgaagccctcattcaacacataaaggacatggtgactcaggcc
   D E A L I Q H I K D M V T Q A
188 tctccatacctgtttgaagctacaggaaaaagattttacttcaaa
   S P Y L F E A T G K R F Y F K
233 aatgttgccatttttgattcccgagagctggaaggcaaagcctgaa
   N V A I L I P E S W K A K P E
278 tatacagggccaaaacttgaaaccttcaaaaacgctgatgtcctt
   Y T R P K L E T F K N A D V L
323 gtatcaacaaccagccctctaggcaatgatgagccctacaccgaa
   V S T T S P L G N D E P Y T E
368 catataggagcatgtggagaaaaaggggatcaggattcacctgact
   H I G A C G E K G I R I H L T
413 cctgacttcttagcaggaaagaagctgactcagtatgggccacaa
   P D F L A G K K L T Q Y G P Q
458 gacaggacctttgtccatgagtgggctcacttccgatggggagtg
   D R T F V H E W A H F R W G V
503 tttaatgaatacaacaacgacgagaagttctacttatccaaagga
   F N E Y N N D E K F Y L S K G
548 aaacccaagcagtgaggtgttcagcagccattaccggtaaaaat
   K P Q A V R C S A A I T G K N
593 caagttcgtcgtgccaggaggagcagttgtatcactaacggaaag
   Q V R R C Q G G S C I T N G K
638 tgtgtaatcgacagagtaacgggactgtataaagacaattgtgta
   C V I D R V T G L Y K D N C V
683 tttgtaccagatccacacaaaaacgagaaggcttccatcatgttt
   F V P D P H Q N E K A S I M F
728 aaccaaataatcaattctgtggttgaattctgtacagaaaaaaat
   N Q N I N S V V E F C T E K N
773 cacaatcaagaagcccaaatgacaaaaaccaacgatgcaatctc
   H N Q E A P N D Q N Q R C N L
818 cgaagcacgtgggaagtcacccaggaatctgaggacttcaagcaa
   R S T W E V I Q E S E D F K Q
863 accactcccatgacagcccagccacctgcacccaccttctcactg
   T T P M T A Q P P A P T F S L
908 ctgcaaattggacaaagaattgtgtgcttagttcttgataagtcc
   L Q I G Q R I V C L V L D K S
953 gggagcatgctgaacgatgatcgctttaaccgaatgaatcaggca
   G S M L N D D R L N R M N Q A
998 agccggcttttctgctgcagactgtggagcagggatcctgggtc
   S R L F L L Q T V E Q G S W V

```


FIG. 2C

2168 caagacaagcagctgtgcttcagcaggacatcttcagggggatcg
Q D K Q L C F S R T S S G G S
2213 tttgtggccaccaatgtccccgcagcagctcccatcctgacctc
F V A T N V P A A A P I P D L
2258 ttccaccctgtcaaatactgacctgaaggccagcatccaaggg
F P P C Q I T D L K A S I Q G
2303 cagaacctggtgaatctgacgtggacggctcctggggatgactac
Q N L V N L T W T A P G D D Y
2348 gaccacgggagagcttccaactacatcatccgaatgagcaccagt
D H G R A S N Y I I R M S T S
2393 atcggtgatctcagggaccacttcaacacctcactccaagtgaac
I V D L R D H F N T S L Q V N
2438 actaccggtcttatcccccagaggccagctctgaggaaatcttt
T T G L I P K E A S S E E I F
2483 gagtttgaactgggaggcaacacttttggaatggcacagatatac
E F E L G G N T F G N G T D I
2528 ttcattgctatccaggctgtggataagtccaatctgaaatcagaa
F I A I Q A V D K S N L K S E
2573 atctccaacattgcacgggtgtctgtgttcacccccgctcaggag
I S N I A R V S V F I P A Q E
2618 ccgcccattcccgaagactcaactcccccttgctcctgacatcagc
P P I P E D S T P P C P D I S
2663 atcaacagcaccattcctggcatccacgtgctgaagataatgtgg
I N S T I P G I H V L K I M W
2708 aagtggttaggggaaatgcaggtgacactaggtttgcactga
K W L G E M Q V T L G L H *

2750 attttcaggcaagaaatcaaccagtcattcctttcactggagaat

2795 tttctaaaaatgtacttttagacttctgtagggggcggtatagta

2840 acactcgaagctgtaaaaactgggtctgggtgcattaaaaattatc

2885 tgttcaaatacaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

2930 aa

FIG. 3A

CLUSTAL W (1.82) sequence alignment of mICACC-1 and bovine CACC (b-CACC)

```

mICACC-1: MESLKSPVFLILHLLEGVLSESLIQLNNNGYEGIVIAIDHDVPEDEALIQHIKDMVTQA 60
b-CACC:  MVPRLTVILFLTLHLLPG-MKSSMVNLINNGYDGIVIAINPSVPEDEKLIQNIKEMVTEA 59

mICACC-1: SPYLFEATGKRIFYFKNVAILIPESWKAKPEYTRPKLETFTKNADVLVSTTSPLGNDEPYTE 120
b-CACC:  STYLFHATKRRVYFRNVSILIPMTWKSSEYLMKQESYDQAEVIVANPYLKHGDDPYTL 119

mICACC-1: HIGACGEKGIRIHLTPDFLAGKKLTQYGPQDRFTVHEWAHFRWGVFNEYNNDEKFYLSK- 179
b-CACC:  QYGRCGEKGQYIHFTPNFLLTNLPIYGSRGRAFVHEWAHLRWGIFDEYNGDQPFYISRR 179

mICACC-1: GKPQAVRCSAAITGKNQVRRRCQGGSCITNGKCVIDRVTGLYKDNCFVDPDPHQNEKASIM 239
b-CACC:  NTIEATRCSTHITGTNVIVKCQGGSCITR-PCRRDSQTGLYEAKCTFIPEKSQTARES IM 238

mICACC-1: FNQNINSVVEFCTEKNHNQEAPNDQNQRCLNSTWEVIEQSEDFKQTTPTMTAQQP--APT 297
b-CACC:  FMQSLHSVTEFCTEKTHNVEAPNLQNKMCNGKSTWDVIMNSTDFQNTSPMTEMNPPTQPT 298

mICACC-1: FSL LQIGQRIVCLVLDKSGSMLNDDRLNRMNQASRLFLLQTVEQGSWVGMVTFDSAAYVQ 357
b-CACC:  FSL LKSKQRVVCLVLDKSGSMSEDRLFRMNQAAELFLIQIIEKGS LVGMVTFDSVAEIR 358

mICACC-1: SELKQLNSGADRDLLIKHLPTVSAGGTSICSGLRTAFT-VIKKKYPTDGSEIVLLTDGED 416
b-CACC:  NNLTKITDDNVYENITANLPQEANGGTSICRGLKAGFQAI IQSQQSTSGSEIILLTDGED 418

mICACC-1: NTISSCFDLVKQSGAIIHTVALGPAAAKELEQLSKMTGGLQTYSSDQVQNNGLVDAFAAL 476
b-CACC:  NEIHSCIEEVKQSGVIIHTIALGPSAAKELETLSDMTGGHRFYANKDIN--GLTNAFSRI 476

mICACC-1: SSGNAAIAQHSIQLESRGVNLQNNQWMNGSVIVDSSVGKDTLFLITWTTHPPTIFIWDPS 536
b-CACC:  SSRSGSITQQTIQLESKALAITKKWVNGTVPVDSTIGNDTFFVVTWTIKKPEILLQDPK 536

mICACC-1: G--VEQNGFILD TT-TKVAYLQVPGTAKVGFWKYSIQ---ASSQTLTLTVTSRAASATLP 590
b-CACC:  GKKYKTSDFKEDKLN IHSARLRIPGIAETGTWYSLNNHASPQILTVTVTTRARSPTTP 596

mICACC-1: PITVTPVVNKNTGKFPSPVTVYASIRQGASPI LRASVTALIESVNGKTVTLELLDNGAGA 650
b-CACC:  PVTATAHMSQNTAHYPSPVIVYAQVSQGFLPVLGINVTAI IETEDGHQV TLELWDNGAGA 656

mICACC-1: DATKNDGVYSRFFTA FDANGRYSVKI WALGGVTS DRQRAAPPKNRAMYIDGWIEDGEVRM 710
b-CACC:  DTVKNDGIYSRYFTDYRGNGRYS LKVHAEARNNTARLSLRQPQN KALYIPGYIENGKIIL 716

mICACC-1: NPPRPETS--YVQDKQLCFSRTSSGGSFVATNVPA AAPIPDLFPPCQITDLKASIQQQNL 768
b-CACC:  NPPRPEVKDDLAKAEIEDFSRLTSGGSFTVSGAPPGN-HPSVLPPNKIIDLEAKFK-EDH 774

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FIG. 3B

mICACC-1: VNLTWTAPGDDYDHGRASNYIIRMSTSIVDLRDHFNTSLQVNTTGLIPKEASSEEIFEFE 828
b-CACC: IQLSWTAPANVLDKGKANSYIIRISKSFLDLQKDFDNATLVNTSSLKPKEAGSDENFEFK 834

mICACC-1: LGGNTFGNGTDIFIAIQAVDKSNLKSEISNIARVSVFIPAQEPPPIPEDSTPPCPDISINS 888
b-CACC: PEPFRIENGNTNFYIAVQAINNEANLTSEVSNIQAIAKFIP-----MPEDSVP-ALGTKISA 888

mICACC-1: TIPGIHVLKIMWKWLGMQVTLGLH 913
b-CACC: INLAIFALAMILSIV----- 903

hICACC-2 Translated Sequence
Sequence Range: 1 to 3190

FIG. 4A1

```
1          cttcttgtgttctttaacccttgcaagtt
30 cagraagaaacccatctgcatccatattgaaaacctgacacaatg
75 tatgcagcaggctcagtgtagtggaactggaggcttctctacaac
120 atgacccaaaggagcattgcaggctcctatTTGCAACCTGAAGTTT
    M T Q R S I A G P I C N L K F
165 gtgactctcctgggtgccttaagttcagaactcccattcctggga
    V T L L V A L S S E L P F L G
210 gctggagtacagcttcaagacaatgggtataatggattgctcatt
    A G V Q L Q D N G Y N G L L I
255 gcaattaatcctcaggtacctgagaatcagaacctcatctcaaac
    A I N P Q V P E N Q N L I S N
300 attaaggaatgataactgaagcttcattttacctattttaatgct
    I K E M I T E A S F Y L F N A
345 accaagagaagagtatTTTTcagaaatataaagattttaataacct
    T K R R V F F R N I K I L I P
390 gccacatggaaagctaataataacagcaaaaataaaacaagaatca
    A T W K A N N N S K I K Q E S
435 tatgaaaaggcaaatgtcatagtgactgactggatatagggcacat
    Y E K A N V I V T D W Y R A H
480 ggagatgatccatacacccctacaatacagagggtgtggaaaagag
    G D D P Y T L Q Y R G C G K E
525 ggaaaatacattcatttcacacctaatttcctactgaatgataac
    G K Y I H F T P N F L L N D N
570 ttaacagctggctacggatcacgaggccgagtgtttgtccatgaa
    L T A G Y G S R G R V F V H E
615 tggggccacctccgttgggggtgtgttcgatgagtataacaatgac
    W A H L R W G V F D E Y N N D
660 aaacctttctacataaatgggcaaaatcaaattaaagtgacaagg
    K P F Y I N G Q N Q I K V T R
705 tgttcacatcgacatcacaggcatttttgtgtgtgaaaaaggctct
    C S S D I T G I F V C E K G P
750 tgcccccaagaaaactgtattattagtaagctttttaagaagga
    C P Q E N C I I S K L F K E G
795 tgcacctttatctacaatagcacccaaagtgcaactgcatcaata
    C T F I Y N S T Q S A T A S I
840 atgttcatgcgaagtttatcttctgtggttgaaatttgtaatgca
    M F M R S L S S V V E F C N A
885 agtaccacacaaccaagaagcaccaaacctacagaaccagatgtgc
    S T H N Q E A P N L Q N Q M C
930 agcctcagaagtgcattgggatgtaatcacagactctgctgacttt
    S L R S A W D V I T D S A D F
975 caccacagctttcccatgaacgggactgagcttccacctcctccc
    H H S F P M N G T E L P P P P
1020 acattctcgctttagaggctgggtgacaaagtggctctgtttagtg
    T F S L V E A G D K V V C L V
```


FIG. 4A2

1065 ctggatgcgtccagcaagatggcagaggctgacagactccttcaa
L D A S S K M A E A D R L L Q
1110 ctacaacaagccgcagaattttatgtgatgcagattgttgaaatt
L Q Q A A E F Y L M Q I V E I
1155 cataccttcgtgggcattgccagtttcgacagcaaaggagagatc
H T F V G I A S F D S K G E I
1200 agagcccagctacaccaaattaacagcaatgatgatcgaaagttg
R A Q L H Q I N S N D D R K L
1245 ctgggtttcataatctgcccaccactgtatcagctaaaacagacatc
L V S Y L P T T V S A K T D I
1290 agcatttgttcagggcttaagaaaggatttgagggtggttgaaaaa
S I C S G L K K G F E V V E K
1335 ctgaatggaaaagcttatggctctgtgatgatattagtgaccagc
L N G K A Y G S V M I L V T S
1380 ggagatgataagcttcttggcaattgcttaccactgtgctcagc
G D D K L L G N C L P T V L S
1425 agtggttcaacaattcactccattgccctgggttcattctgcagcc
S G S T I H S I A L G S S A A
1470 ccaaactctggaggaattatcacgtcttacaggaggtttaaagtcc
P N L E E L S R L T G G L K F
1515 tttgttccagatatatcaaaactccaatagcatgattgatgctttc
F V P D I S N S N S M I D A F
1560 agtagaattttcctctggaactggagacattttccagcaacatatt
S R I S S G T G D I F Q Q H I
1605 cagcttgaaagtacaggtgaaaatgtcaaacctcaccatcaattg
Q L E S T G E N V K P H H Q L
1650 aaaaacacagtgactgtggataatactgtgggcaacgacactatg
K N T V T V D N T V G N D T M
1695 tttctagttacgtggcaggccagtggtcctcctgagattatatta
F L V T W Q A S G P P E I I L
1740 tttgatcctgatggacgaaaatactacacaaataattttatcacc
F D P D G R K Y Y T N N F I T
1785 aatctaacttttcggacagctagtctttggattccaggaacagct
N L T F R T A S L W I P G T A
1830 aagcctgggcactggacttacaccctgaacaatacccatcattct
K P G H W T Y T L N N T H H S
1875 ctgcaagccctgaaagtgacagtgacctctcgtgcctccaactca
L Q A L K V T V T S R A S N S
1920 gctgtgccccagccactgtggaagcctttgtggaaagagacagc
A V P P A T V E A F V E R D S
1965 ctccattttcctcatcctgtgatgatttatgccaatgtgaaacag
L H F P H P V M I Y A N V K Q
2010 ggatttttatcccatttctaataatgccactgtcactgccacagttgag
G F Y P I L N A T V T A T V E
2055 ccagagactggagatcctgttacgctgagactccttgatgatgga
P E T G D P V T L R L L D D G
2100 gcaggtgctgatgttataaaaaatgatggaatttactcgaggtat
A G A D V I K N D G I Y S R Y
2145 tttttctcctttgctgcaaatggtagatatagcttgaaagtgcat
F F S F A A N G R Y S L K V H

FIG. 4A3

2190 gtcaatcactctcccagcataagcacccccagcccactctattcca
V N H S P S I S T P A H S I P
2235 gggagtcattgctatgtatgtaccagggttacacagcaaacggtaat
G S H A M Y V P G Y T A N G N
2280 attcagatgaatgctccaaggaaatcagtaggcagaaatgaggag
I Q M N A P R K S V G R N E E
2325 gagcgaaaagtggggcttttagccgagtcagctcaggaggctccttt
E R K W G F S R V S S G G S F
2370 tcagtgtctgggagttccagctggccccaccctgatgtgtttcca
S V L G V P A G P H P D V F P
2415 ccatgcaaaattattgacctggaagctgtaaaagtagaagaggaa
P C K I I D L E A V K V E E E
2460 ttgaccctatcttggacagcacctggagaagactttgatcagggc
L T L S W T A P G E D F D Q G
2505 caggctacaagctatgaaataagaatgagtaaaagtctacagaat
Q A T S Y E I R M S K S L Q N
2550 atccaagatgactttaacaatgctatttttagtaaatacatcaaag
I Q D D F N N A I L V N T S K
2595 cgaaatcctcagcaagctggcatcagggagatatttacgttctca
R N P Q Q A G I R E I F T F S
2640 cccagatttccacgaatggacctgaacatcagccaaatggagaa
P Q I S T N G P E H Q P N G E
2685 acacatgaaagccacagaatttatgttgcaatacagagcaatggat
T H E S H R I Y V A I R A M D
2730 aggaactccttacagtctgctgtatctaacattgccaggcgct
R N S L Q S A V S N I A Q A P
2775 ctgtttattcccccaattctgatcctgtacctgccagagattat
L F I P P N S D P V P A R D Y
2820 cttatattgaaaggagttttaacagcaatgggtttgataggaatc
L I L K G V L T A M G L I G I
2865 atttgccttattatagttgtgacacatcatactttaagcaggaaa
I C L I I V V T H H T L S R K
2910 aagagagcagacaagaaagagaatggaacaaaattattataa
K R A D K K E N G T K L L *

2952 ataaatatccaaagtgtcttccttcttagatataagacccatggc

2997 cttcgactacaaaaacataactaaciaaagtcaaattaacatcaaaa

3042 ctgtattaaaatgcattgagttttgtacaatacagataagatttt

3087 tacatggtagatcaacaaattctttttgggggtagattagaaaac

3132 cttacacttttggctatgaacaaataataaaaattattctttaaaa

3177 aaaaaaaaaaaaaa 3190

FIG. 4B1

hICACC-1

Sequence Range: 1 to 2745

```
1 atggggccattttaagagttctgtgttcaccttgattcttcacctt
  M G P F K S S V F T L I L H L
46 ctagaaggggcccctgagtaattcactcattcagctgaacaacaat
  L E G A L S N S L I Q L N N N
91 ggctatgaaggcattgtcgttgcaatcgaccccaatgtgccagaa
  G Y E G I V V A I D P N V P E
136 gatgaaacactcattcaacaaataaaggacatggtgacccaggca
  D E T L I Q Q I K D M V T Q A
181 tctctgtatctgtttgaagctacaggaaagcgattttattttcaaa
  S L Y L F E A T G K R F Y F K
226 aatggttgccattttgattcctgaaacatggaagacaaaggctgac
  N V A I L I P E T W K T K A D
271 tatgtgagacaaaacttgagacctacaaaaatgctgatgttctg
  Y V R P K L E T Y K N A D V L
316 gttgctgagtctactcctccaggaatgatgaaccctacactgag
  V A E S T P P G N D E P Y T E
361 cagatgggcaactgtggagagaaggggtgaaaggatccacctcact
  Q M G N C G E K G E R I H L T
406 cctgatttcattgcaggaaaaaagttagctgaatatggaccacaa
  P D F I A G K K L A E Y G P Q
451 ggtagggcattttgtccatgagtgggctcatctacgatggggagta
  G R A F V H E W A H L R W G V
496 tttgacgagtacaataatgatgagaaattctacttatccaatgga
  F D E Y N N D E K F Y L S N G
541 agaatacaagcagtaagatgttcagcaggtattactggtacaaat
  R I Q A V R C S A G I T G T N
586 gtagtaaaagaagtgtcagggaggcagctgttacaccaaaaagatgc
  V V K K C Q G G S C Y T K R C
631 acattcaataaagtwacaggactctatgaaaaaggatgtgagttt
  T F N K V T G L Y E K G C E F
676 gttctccaatcccgcagacggagaaggcttctataatgtttgca
  V L Q S R Q T E K A S I M F A
721 caacatgtttgattctatagttgaattctgtacagaacaaaaccac
  Q H V D S I V E F C T E Q N H
766 aacaaagaagctccaaacaagcaaaaatcaaaaatgcaatctccga
  N K E A P N K Q N Q K C N L R
811 agcacatgggaagtgatccgtgattctgaggactttaagaaaacc
  S T W E V I R D S E D F K K T
856 actcctatgacaacacagccaccaaatacccaccttctcattgctg
  T P M T T Q P P N P T F S L L
901 cagattggacaaaagaattgtgtgttttagtccttgacaaatctgga
  Q I G Q R I V C L V L D K S G
946 agcatggcgactggtaaccgcctcaatcgactgaatcaagcaggc
  S M A T G N R L N R L N Q A G
991 cagcttttctgctgcagacagttgagctgggggtcctggggtggg
  Q L F L L Q T V E L G S W V G
1036 atggtgacatttgacagtgctgcccattgtacaaagtgaactcata
  M V T F D S A A H V Q S E L I
1081 cagataaacagtggtcagtgacagggacacactcgccaaaagatta
  Q I N S G S D R D T L A K R L
1126 cctgcagcagcttcaggaggagcgtccatctgcagcgggcttoga
  P A A A S G G T S I C S G L R
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FIG. 4B2

1171 tcggcattttactgtgattaggaagaaatatccaactgatggatct
S A F T V I R K K Y P T D G S
1216 gaaattgtgctgctgacggatggggaagacaacactataagtggg
E I V L L T D G E D N T I S G
1261 tgctttaacgaggtcaaacaaagtgggtgccatcatccacacagtc
C F N E V K Q S G A I I H T V
1306 gcttttggggccctctgcagctcaagaactagaggagctgtccaaa
A L G P S A A Q E L E E L S K
1351 atgacaggaggtttacagacatatgcttcagatcaagttcagaac
M T G G L Q T Y A S D Q V Q N
1396 aatggcctcattgatgcttttggggccctttcatcaggaaatgga
N G L I D A F G A L S S G N G
1441 gctgtctctcagcgcctccatccagcttgagagtaagggattaacc
A V S Q R S I Q L E S K G L T
1486 ctccagaacagccagtgatgaatggcacagtgatcgtggacagc
L Q N S Q W M N G T V I V D S
1531 accgtgggaaaggacactttgtttcttatcacctggacaacgcag
T V G K D T L F L I T W T T Q
1576 cctcccaaatccttctctgggatcccagtggaacagaagcaaggt
P P Q I L L W D P S G Q K Q G
1621 ggctttgtagtggacaaaaacacccaaatggcctacctccaaatc
G F V V D K N T K M A Y L Q I
1666 ccaggcattgctaagggttgacacttggaatacagtcctgcaagca
P G I A K V G T W K Y S L Q A
1711 agctcacaaaccttgaccctgactgtcacgtcccgtgcgtccaat
S S Q T L T L T V T S R A S N
1756 gctaccctgcctccaattacagtgacttccaaaacgaacaaggac
A T L P P I T V T S K T N K D
1801 accagcaaattccccagccctctggtagtttatgcaaatattcgc
T S K F P S P L V V Y A N I R
1846 caaggagcctcccaattctcagggccagtggtcacagccctgatt
Q G A S P I L R A S V T A L I
1891 gaatcagtgaatggaaaaacagttaccttggaaactactggataat
E S V N G K T V T L E L L D N
1936 ggagcaggtgctgatgctactaaggatgacgggtgtctactcaagg
G A G A D A T K D D G V Y S R
1981 tatttcacaacttatgacacgaatggtagatacagtgtaaaagtg
Y F T T Y D T N G R Y S V K V
2026 cgggctctgggaggagttaacgcagccagacggagagtataccc
R A L G G V N A A R R R V I P
2071 cagcagagtggagcactgtacatacctggctggattgagaatgat
Q Q S G A L Y I P G W I E N D
2116 gaaatccaatggaatccaccaagacctgaaattaataaggatgat
E I Q W N P P R P E I N K D D
2161 gttcaacacaagcaagtgtgtttcagcagaacatcctcgggaggg
V Q H K Q V C F S R T S S G G
2206 tcatttgtggcttctgatgtcccaaatgctcccatacctgatctc
S F V A S D V P N A P I P D L
2251 ttcccacctggccaaatcaccgacctgaaggcggaattcacggg
F P P G Q I T D L K A E I H G
2296 ggcagtctcattaatctgacttggacagctcctggggatgattat
G S L I N L T W T A P G D D Y
2341 gaccatggaacagctcacaaagtatatcattcgaataagtacaagt
D H G T A H K Y I I R I S T S

FIG. 4B3

2386 attcttgatctcagagacaagttcaatgaatctcttcaagtgaat
I L D L R D K F N E S L Q V N
2431 actactgctctcatcccaaaggaagccaactctgaggaagtcttt
T T A L I P K E A N S E E V F
2476 ttgttttaaacagaaaacattacttttgaaaatggcacagatctt
L F K P E N I T F E N G T D L
2521 ttcattgctattcaggctgttgataaggctcgatctgaaatcagaa
F I A I Q A V D K V D L K S E
2566 atatccaacattgcacgagtatctttgtttattcctccacagact
I S N I A R V S L F I P P Q T
2611 ccgccagagacacctagtcctgatgaaacgtctgctccttgctcct
P P E T P S P D E T S A P C P
2656 aatattcatatcaacagcaccattcctggcattcacatttttaaaa
N I H I N S T I P G I H I L K
2701 attatgtggaagtggataggagaactgcagctgtcaatagcctag 2745
I M W K W I G E L Q L S I A *

FIG. 5A

CLUSTAL W (1.82) multiple sequence alignment of mouse and human ICACC proteins

```

mICACC-1: --MESLKSPVFLILHLLEGVLSESL-----IQLNNNGYEGIVIAIDHDVPEDEALIQH 52
hICACC-1  --MGPFKSSVFILILHLLEGALSNSL-----IQLNNNGYEGIVVAIDPNVPEDETLIQQ 52
hICACC-2: MTQRSIAGPICNLKFVTLVALSSELPLFLGAGVQLQDNGYNGLLIAINPQVPENQNLISN 60

mICACC-1: IKDMVTQASPYLFEATGKRFYFKNVAILIPESWKAKPEYTRPKLETFTKNADVLVSTTSPL 112
hICACC-1: IKDMVTQASLYLFEATGKRFYFKNVAILIPETWKTADYVRPKLETYKNADVLVAESTPP 112
hICACC-2: IKEMITEASFYLFNATKRRVFFRNIKILIPATWKAN-NNSKIKQESYEKANVIVTDWYRA 119

mICACC-1: GNDEPYTEHIGACGEKGIRIHLTPDFLAGKKLTQ-YGPQDRTFVHEWAHFRWGVFNEYNN 171
hICACC-1: GNDEPYTEQMGNCGEKGGERIHLTPDFIAGKKLAE-YGPQGRAFVHEWAHLRWGVFDEYNN 171
hICACC-2: HGDDPYTLQYRGCCKEGKYIHFTPNFLLNDNLTAGYGSRRGRVVFHEWAHLRWGVFDEYNN 179

mICACC-1: DEKFYLS-KGKPQAVRCSAAITGKNQVRRCCGGSCITNGKCVIDRVTGLYKDNCVFPDP 230
hICACC-1: DEKFYLS-NGRIQAVRCSAGITGTNVVKKCCGGSCYTK-RCTFNKXTGLYEKGCEFLVQS 229
hICACC-2: DKPFYINGQNQIKVTRCSSDITG---IFVCEKGPQPQE-NCIISK---LFKEGCTFIYNS 232

mICACC-1: HQNEKASIMFNQNINSVVEFCTEKNHNQEAPNDQNQRCLNRSTWEVIEQESDFKQTTTPM- 289
hICACC-1: RQTEKASIMFAQHVDSEIVEFCTEQNHNEAPNKQNKCNLRSTWEVIRDSDFKKTTPM- 288
hICACC-2: TQSATASIMFMRLSSVVEFCNASTHNQEAPNLQNMCSLRSALWDVITDSADFHHSFPMN 292

mICACC-1: -TAQPPAPTFSLLQIGQRIVCLVLDKSGSMLNDDRNLNRMNQASRLFLLQTVEQGSWVGMV 348
hICACC-1: -TTQPPNPFTFSLLQIGQRIVCLVLDKSGSMATGNRLNRLNQAGQLFLLQTVELGSWVGMV 347
hICACC-2: GTELPPPPTFSLVEAGDKVVCVLVDASSKMAEADRLQLQQAEEFYLMQIVEIHTFVGIA 352

mICACC-1: TFDSAAYVQSELKQLNSGADRDLLIKHLPTVSAGGT--SICSGLRTAFTVIKKKY-PTDG 405
hICACC-1: TFDSAHHVQSELIQINSGLSDRDTLAKRLPAAASGGT--SICSGLRSFTVIRKKY-PTDG 404
hICACC-2: SFDSKGEIRAQLHQINSNDDRKLLVSYLPTTVSAKTDISICSGLKKGFVVEKLNKGAYG 412

mICACC-1: SEIVLLTDGEDNTISSCFDLVKQSGAIIHTVALGPAAAKELEQLSKMTGGLQTYSSDQVQ 465
hICACC-1: SEIVLLTDGEDNTISGCFNEVKQSGAIIHTVALGPSAAQEELELSKMTGGLQTYASDQVQ 464
hICACC-2: SVMILVTSGDDKLLGNCLPTVLSSGSTIHSIALGSSAAPNLEELSRLTGGLKFFVDPDISN 472

mICACC-1: NNGLVDAFAALSSGNAAIAQHSIQLESRGVNLQNNQWMNGSVIVDSSVGKDTLFLITWTT 525
hICACC-1: NNGLIDAFGALSSGNAAVQSRSIQLESKGLTLQNSQWMNGTVIVDSTVGKDTLFLITWTT 524
hICACC-2: SNSMIDAFSRISSTGDIQQHIQLESTGENVKPHHQLKNTVTVDNTVGNMTMFLVTWQA 532

mICACC-1: H-PPTIFIWDPSGVE--QNGFILDTTTKVAYLQVPGTAKVGFWKYSIQ---ASSQTLTLT 579
hICACC-1: Q-PPQILLWDPSGQK--QGGFVVDKNTKMAYLQIPGIAKVGTWKYSLQ---ASSQTLTLT 578
hICACC-2: SGPPEIILFDPDGRKYTYNNFITNLTFRTASLWIPGTAKPGHWYTLNNTTHSLQALKVT 592

```

FIG. 5B

mICACC-1: VTSRAASATLPPITVTPVVNKNKGKFPSPVTVYASIRQGASPILRASVTALIESVNGKTV 639
hICACC-1: VTSRASNATLPPITVTSKTNKDTSKFPSPLVVYANIRQGASPILRASVTALIESVNGKTV 638
hICACC-2: VTSRASNSAVPPATVEAFVERDSLHFPHPVMIYANVKQGFYPILNATVTATVEPETGDPV 652

mICACC-1: TLELLDNGAGADATKNDGVYSRFFTAFDANGRYSVKIWALGGVTSRQRAAPPKNRAMYI 699
hICACC-1: TLELLDNGAGADATKDDGVYSRYFTTYDTNGRYSVKVRALGGVNAARRRVIPQQSGALYI 698
hICACC-2: TLRLDDGAGADVIKNDGIYSRYFFSFAANGRYSLKVHVNHSPSISTPAHSIPGSHAMYV 712

mICACC-1: DGWIEDGEVRMNPFRPETS--YVQDKQLCFSTRSSGGSFVATNPVAAAPIPDLFPPCQIT 757
hICACC-1: PGWIENDEIQWNPPRPEINKDDVQHKQVCFSRTSSGGSFVASDVPN-APIPDLFPPGQIT 757
hICACC-2: PGYTANGNIQMNAPRKS VGR-NEEERKWGFSRVSSGGSFVSLGVPA-GPHPDVFPPCKII 770

mICACC-1: DLKASIQGQNLVNLWTAPGDDYDHGRASNYIIRMSTSIVDLRDHFNTSLQVNTTGLIPK 817
hICACC-1: DLKAEIHGGSLINLTWTAPGDDYDHGTAHKYIIRISTSIILDLRDKFNESLQVNTTALIPK 817
hICACC-2: DLEAVKVEBELT-LSWTAPGEDFDQQAQTSYEIRMSKSLQNIQDDFNAILVNTSKRNPQ 829

mICACC-1: EASSEEIFEFELGGNTFG-----NG-----TDIFIAIQAVDKSNLKSEISNIARVSFIP 867
hICACC-1: EANSEEVFLFKPENITFE-----NG-----TDLFIAIQAVDKVDLKSEISNIARVSLFIP 867
hICACC-2: QAGIREIFTFSPQISTNGPEHQPNGETHESHRIYVAIRAMDRNSLQSAVSNIAQAPLFIP 889

mICACC-1: AQEP---PIPEDSTPPCPDISINSTIPGIHVLKIMWKWLGEMQVTLGLH----- 913
hICACC-1: PQTPPETPSPDETSAPCPNIHINSTIPGIHILKIMWKWIGELQLSIA----- 914
hICACC-2: PNSD---PVPARDYLILKGVLTA MGLIGIICLIIVVTHHTLSRKKRADKKENGTKLL 943

FIG. 6

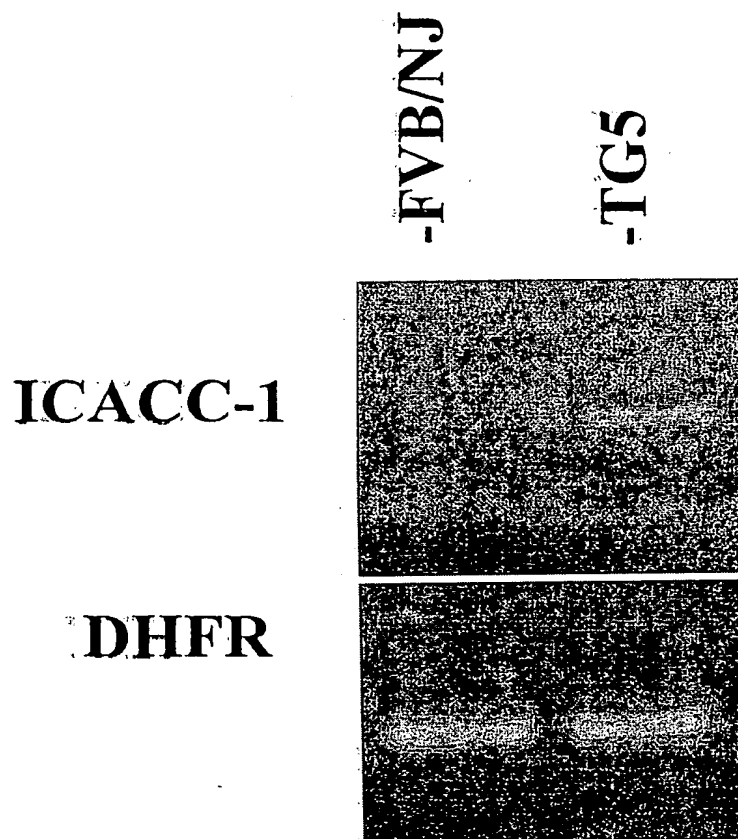


FIG. 7

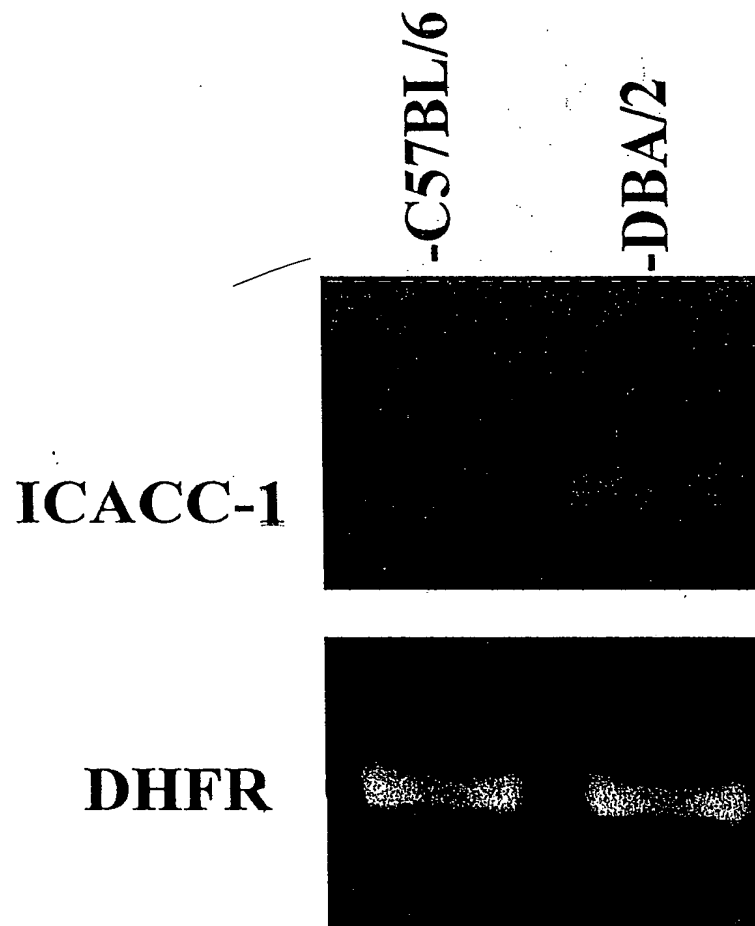
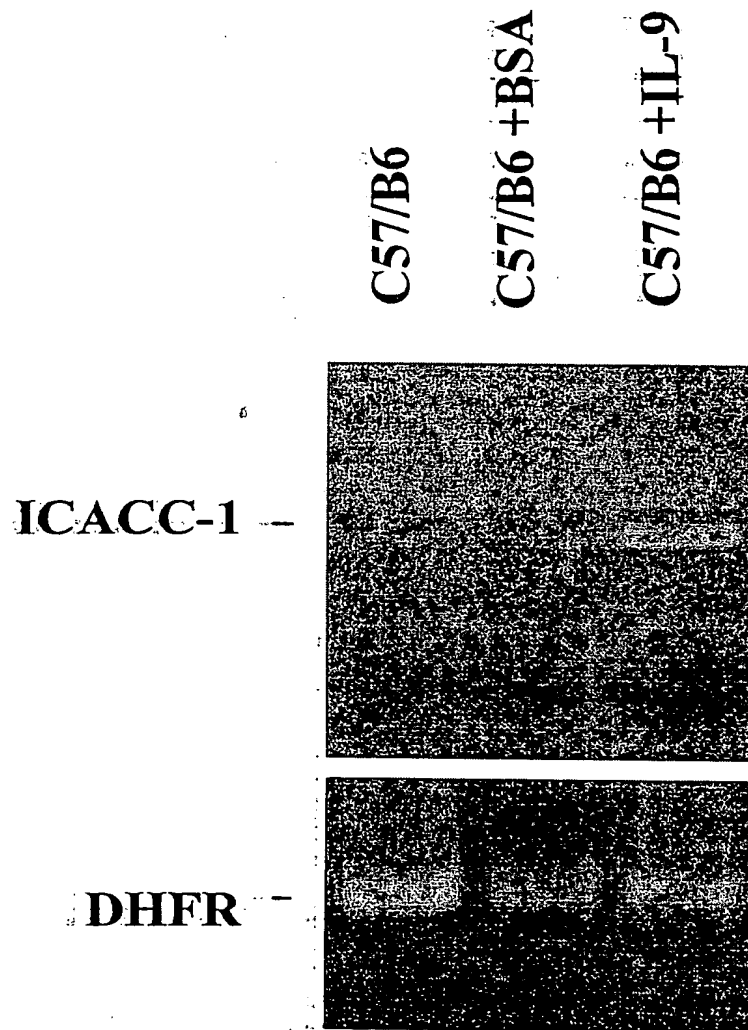


FIG. 8



IL-9 Transgenic Mouse

1. uterus
2. thymus
3. testis
4. stomach
5. Spleen
6. sml. intestine
7. ovary
8. muscle
9. lymph nodes
10. lung
11. liver
12. kidney
13. heart
14. colon
15. brain



FIG. 9A

Normal Mouse

1. heart
2. brain
3. spleen
4. lung
5. liver
6. skeletal muscle
7. kidney
8. testis

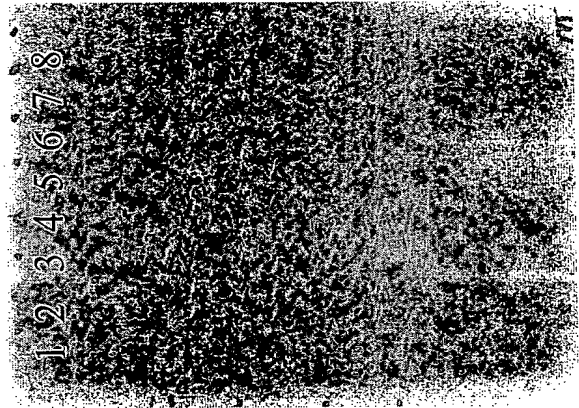


FIG. 9B

FIG. 10A

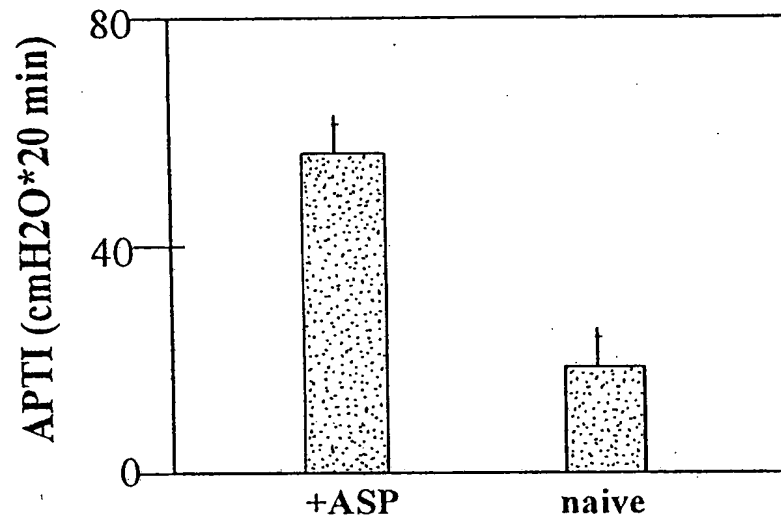


FIG. 10B

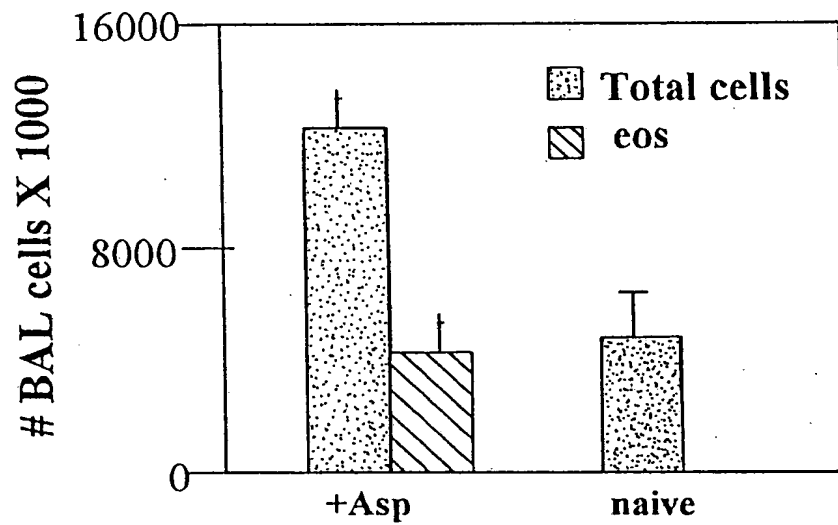


FIG. 11

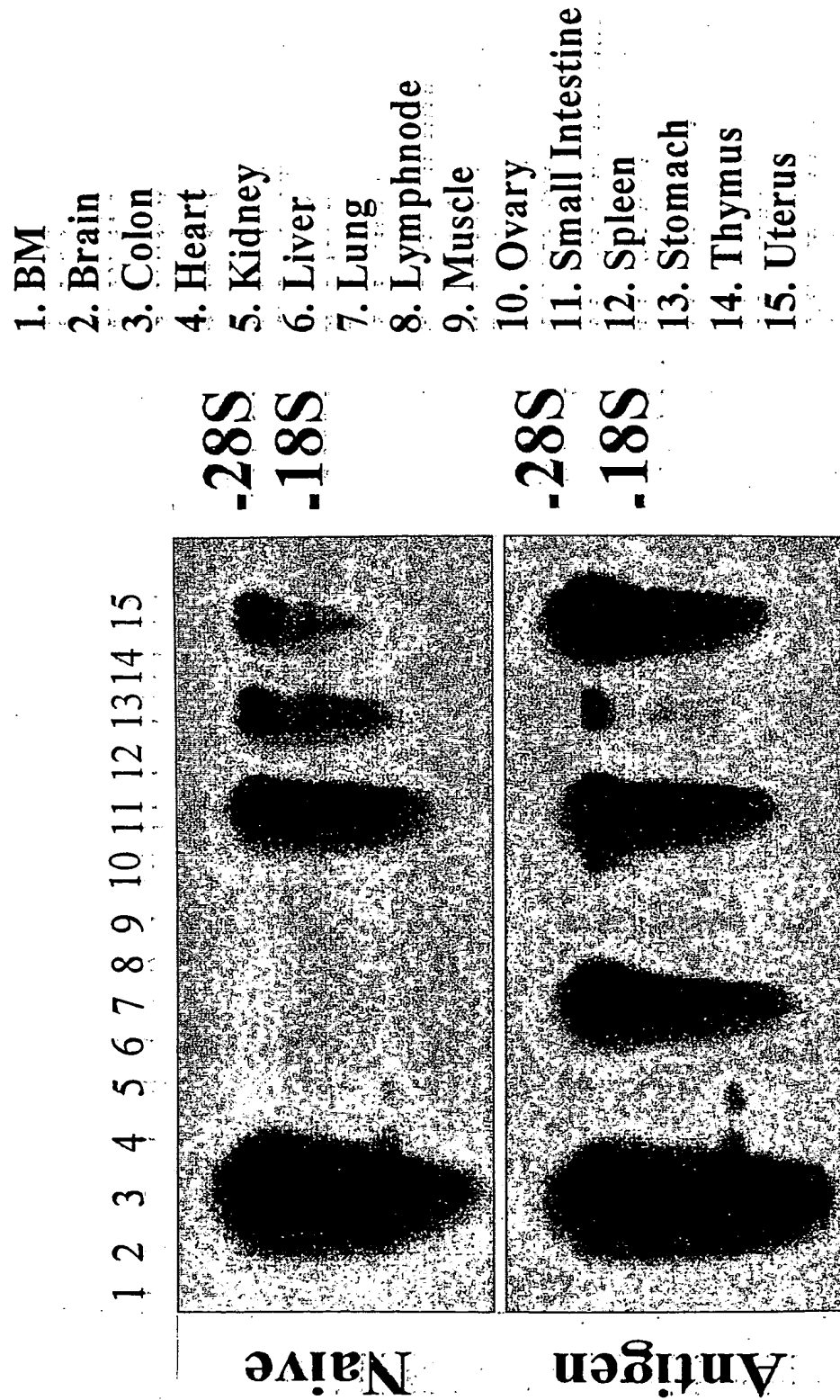


FIG. 12A

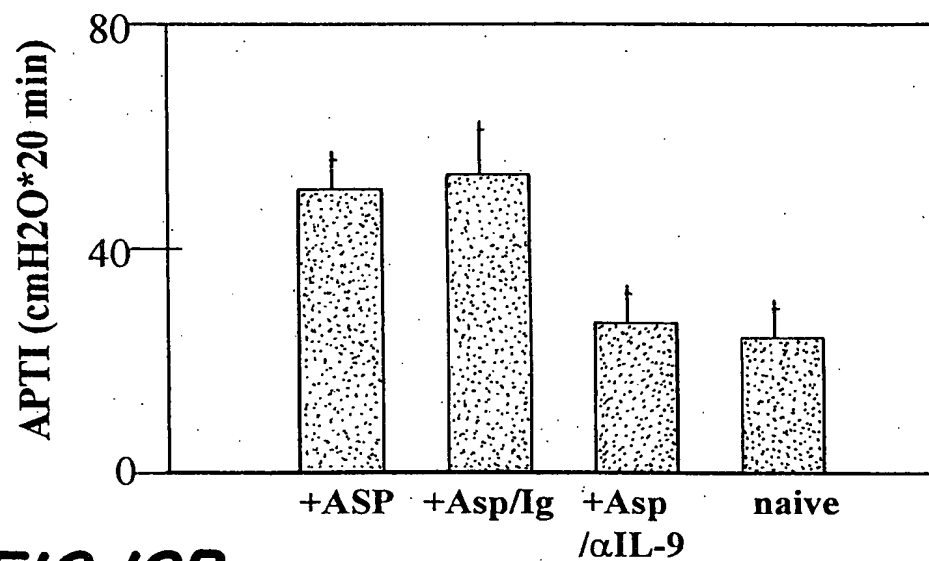


FIG. 12B

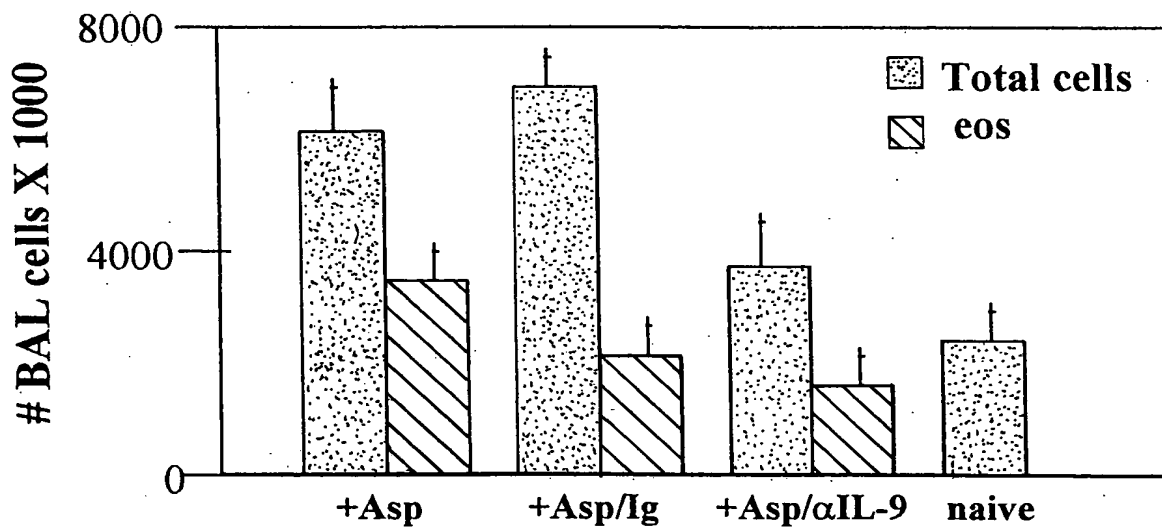


FIG. 13

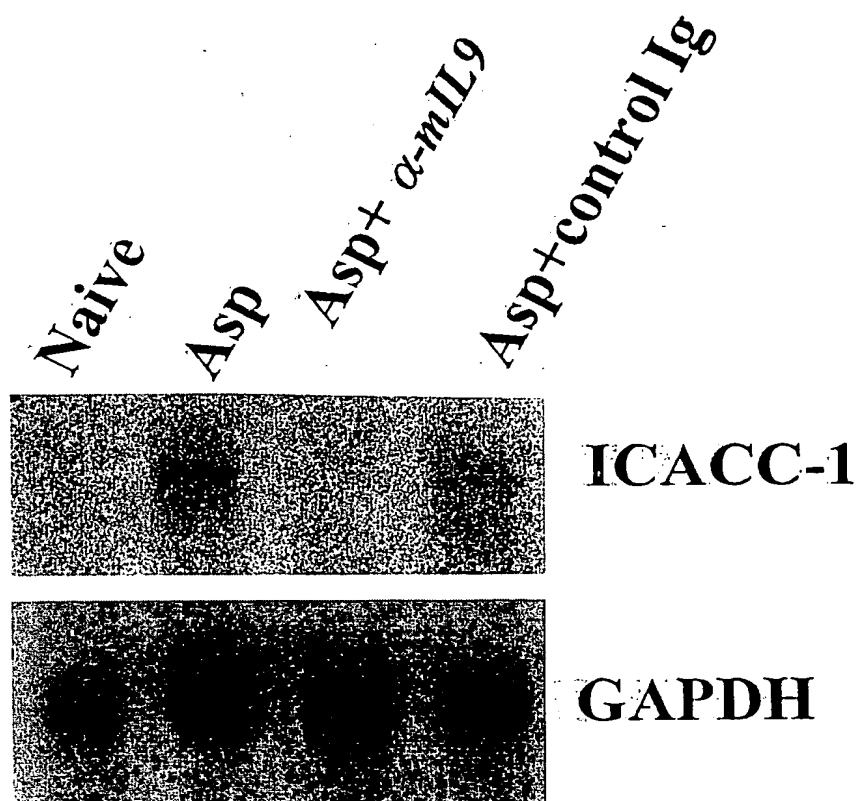


FIG. 14

NHBE

- IL-9

hICACC-1

γ -Actin

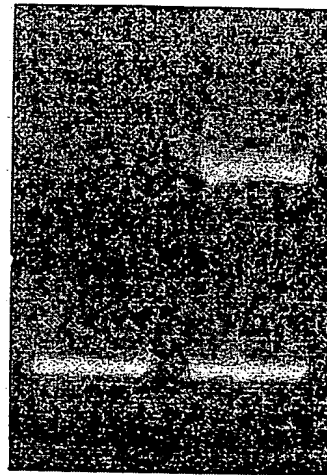
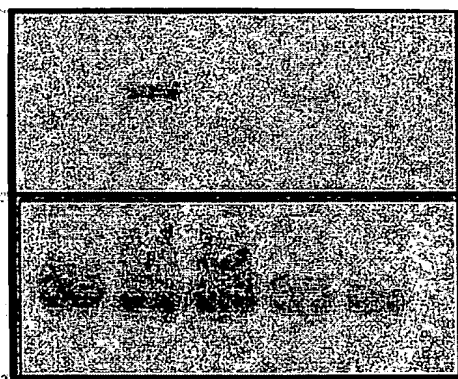


FIG. 15

Patient

1 2

hIL-9 - + - + c



hICACC-1

hPMS2

FIG. 16

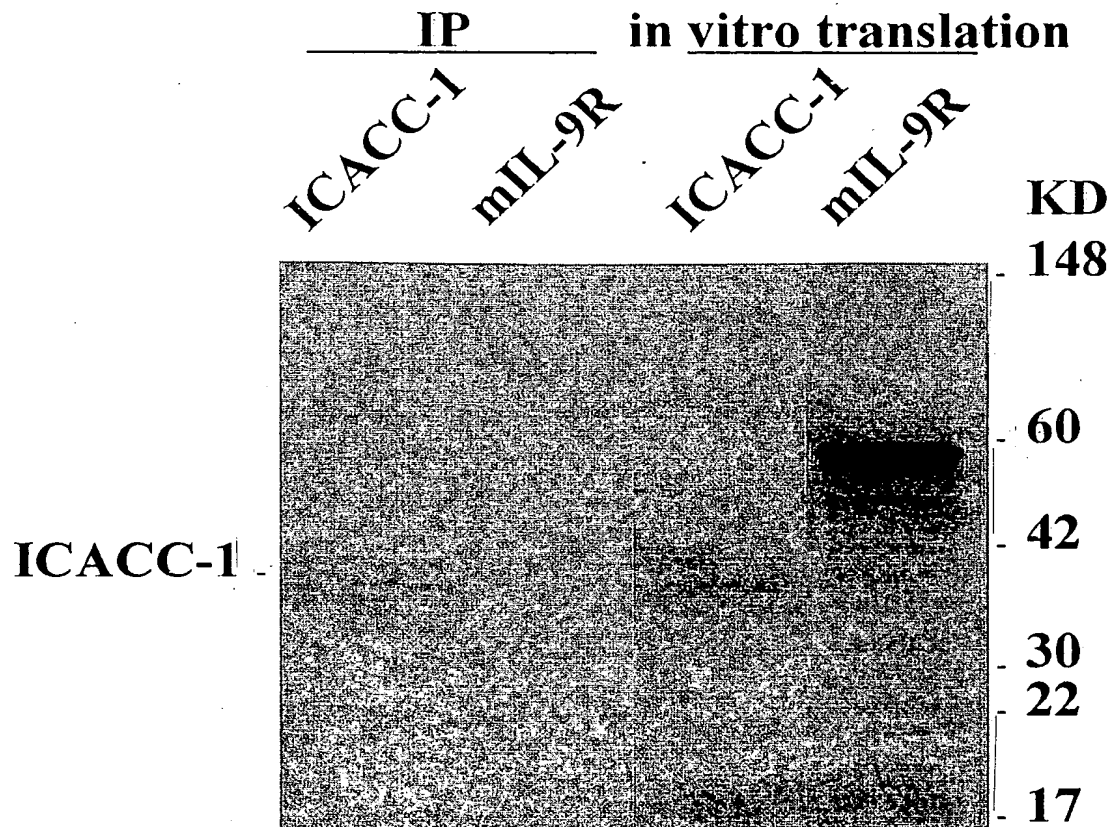


FIG. 17

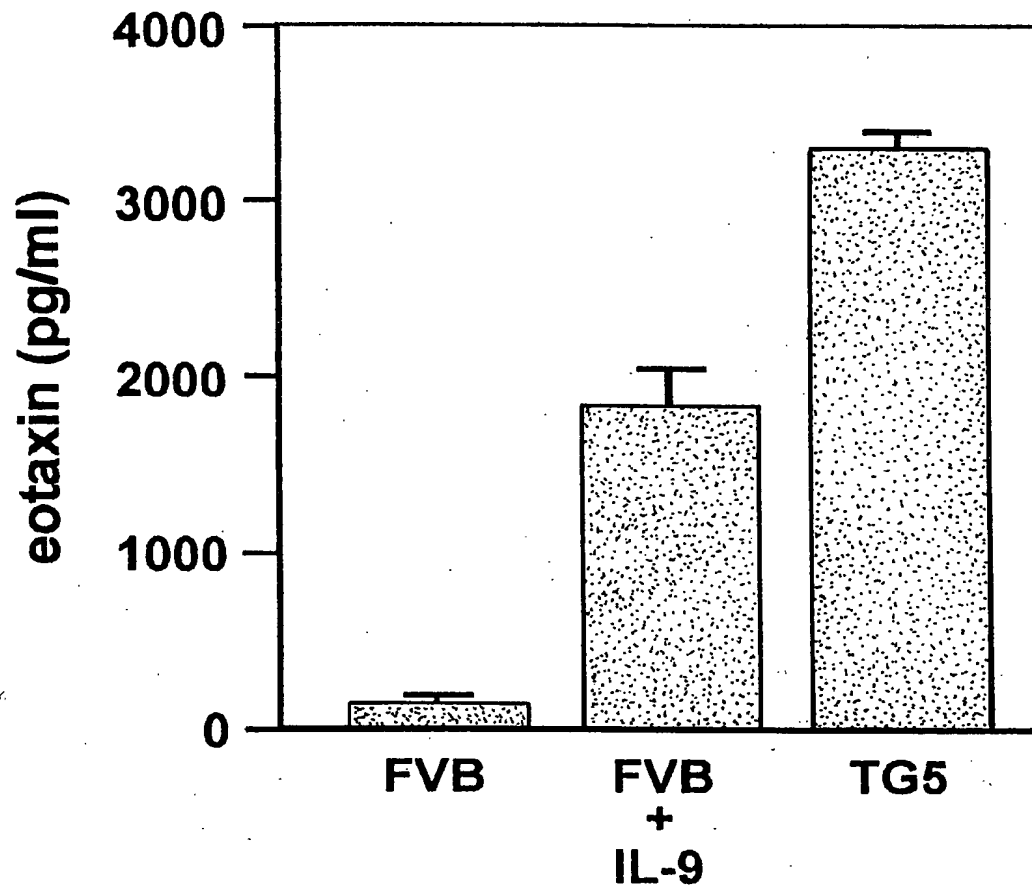


FIG. 18

